## WHAT IS CLAIMED IS:

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- 3 1. A method for detection of at least one allele of a genetic locus comprising amplifying genomic DNA 4 with an intron-spanning primer pair that defines a 5 6 DNA sequence, said DNA sequence being in genetic 7 linkage with said genetic locus and containing a 8 sufficient number of intron sequence nucleotides 9 to produce an amplified DNA sequence 10 characteristic of said allele.
- 11 2. The method of Claim 1 wherein said amplified DNA 12 sequence includes at least about 300 nucleotides 13 corresponding to intron sequences.
  - 3. The method of Claim 1 wherein said intron sequence is adjacent to an exon encoding said allele.
    - 4. The method of Claim 1 wherein said amplified DNA sequence is characteristic of at least one nonadjacent allele.
    - 5. The method of Claim 1 wherein said amplified DNA sequence is characteristic of at least one adjacent allele and at least one nonadjacent allele.
    - 6. The method of Claim 5 wherein said amplified DNA sequence includes at least about 1,000 nucleotides corresponding to intron sequences.
    - 7. A method for detection of at least one allele of a genetic locus comprising:
      - a. amplifying genomic DNA with an intronspanning primer pair that defines a DNA
        sequence, said DNA sequence being in genetic
        linkage with said allele and containing a
        sufficient number of intron sequence
        nucleotides to produce an amplified DNA
        sequence characteristic of said allele; and

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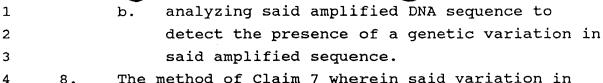
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- 8. The method of Claim 7 wherein said variation in said amplified DNA sequence is a variation in the length of the primer-defined amplified DNA sequence.
- 9. The method of Claim 7 wherein said variation in said amplified DNA sequence is a change in the presence of at least one restriction site in the primer-defined amplified DNA sequence.
- 12 10. The method of Claim 7 wherein said variation in 13 said amplified DNA sequence is a change in the 14 location of at least one restriction site in the 15 primer-defined amplified DNA sequence.
  - 11. The method of Claim 7 wherein said variation in said amplified DNA sequence is a substitution of at least one nucleotide in the primer-defined amplified DNA sequence.
- 20 12. The method of Claim 7 wherein said genetic locus 21 is a major histocompatibility locus.
- 22 13. The method of Claim 7 wherein said allele is 23 associated with a monogenic disease.
  - 14. The method of Claim 13 wherein said monogenic disease is cystic fibrosis.
- 26 15. The method of Claim 7 wherein at least about 70% of said primer-defined amplified DNA sequence corresponds to intron sequences.
- The method of Claim 7 wherein said primer-defined amplified DNA sequence is from 300 to 500 nucleotides in length.
- 32 17. A method for producing RFLP fragments for an HLA 33 locus of an individual comprising the steps of:
- a. amplifying genomic HLA DNA from said individual with a primer pair specific for

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1		said HLA locus under conditions suitable to
2		produce an amplified DNA sequence; and
3		<ul> <li>b. producing a digest by combining said</li> </ul>
4		amplified DNA sequence with at least one
5		endonuclease that cleaves said amplified DNA
6		sequence to yield a set of fragments having
7		distinctive fragment lengths.
8	18.	The method of Claim 17 additionally comprising the
9		step of producing RFLP patterns from said digest.
10	19.	The method of Claim 17 wherein said primers define
11		a DNA sequence that contains all exons that encode
1.2		allelic variability associated with said HLA
13		locus.
14	20.	A method for producing RFLP fragments for an HLA
15		locus of an individual comprising the steps of:
16		a. amplifying genomic HLA DNA from said
17		individual with a primer pair specific for
18		said HLA locus under conditions suitable to
19		produce an amplified DNA sequence, said
20		primers defining a DNA sequence that contains
21		all exons that encode allelic variability
22		associated with said HLA locus; and
23		b. producing a digest by combining said
24		amplified DNA sequence with at least one
25		endonuclease that cleaves said amplified DNA
26		sequence to yield a set of fragments having
27		distinctive fragment lengths.
28	21.	A method for producing RFLP patterns for an HLA
29		locus of an individual comprising the steps of:
30		a. amplifying HLA DNA from said individual with
31		a primer pair specific for said HLA locus
32		under conditions suitable to produce an
33		amplified DNA sequence, said primers being
34		located in intervening sequence I and in
35		intervening sequence III when said HLA locus

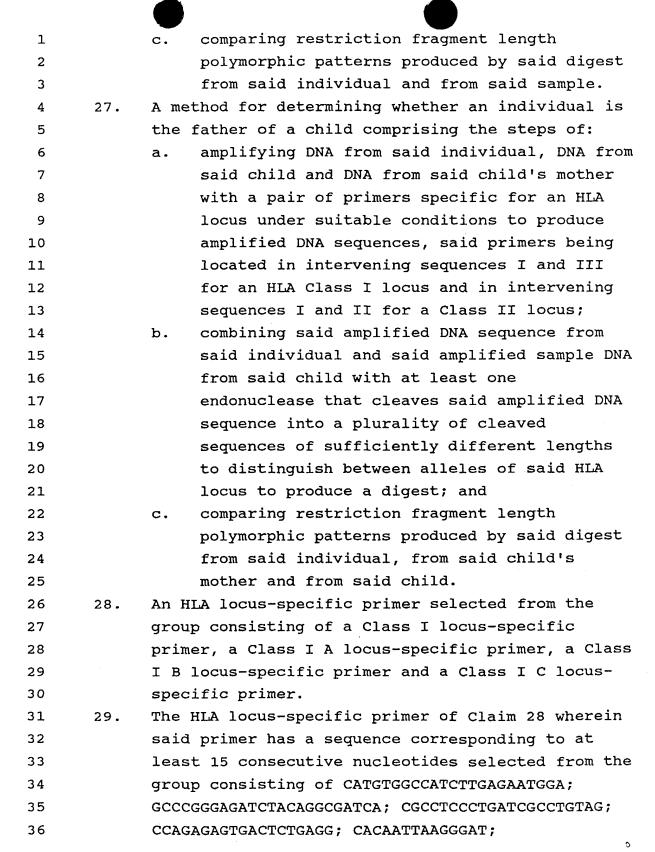
is a Class I locus and in intervening

1		sequence I and in intervening sequence II
2		when said locus is a Class II locus;
3		b. producing a digest by combining said
4		amplified DNA sequence with at least one
5		endonuclease that cleaves said amplified DNA
6		sequence to yield a set of fragments having
7		distinctive fragment lengths; and
8		c. producing RFLP patterns from said digest.
9	22.	The method of Claim 21 wherein said amplification
10		comprises:
11		a. combining an HLA-locus specific primer pair
12		with HLA DNA from said individual under
13		hybridizing conditions for a period of time
14		sufficient for each primer in said primer
15		pair to produce an extension product which,
16		when separated from its complement, can serve
17		as a template for synthesis of the extension
18		product of the other primer to produce a
19		mixture;
20		b. treating said mixture under denaturing
21		conditions to separate the primers from their
22		extension products;
2:3		c. treating said mixture with said HLA locus-
24		specific primer pair such that a primer
25		extension product is synthesized using each
26		of the templates produced in step (b) as a
27		template, resulting in amplification of the
28		HLA DNA; and
29		d. repeating steps (b) and (c) to produce an
30		amplified DNA sequence.
31	23.	The method of Claim 21 wherein a second primer
32		pair specific for said HLA locus is also used to
33		amplify said HLA DNA.
34	24.	The method of Claim 21 wherein producing said RFLP

fragment pattern comprises:

1		a. combining said amplified DNA sequence with at
2		least one endonuclease that cleaves said
3		amplified DNA sequence to yield a set of
4		fragments having distinctive fragment
5		lengths;
6		b. separating said fragments based on the length
7		of the fragments to produce separated
8		fragments; and
9		c. visualizing said separated fragments to
10		produce RFLP fragment patterns.
11	25.	The method of Claim 24 wherein said fragments are
12		separated using gel electrophoresis and visualized
13		using a nucleotide-specific stain.
14	26.	A method for determining whether DNA in a sample
15		is from a particular individual comprising the
16		steps of:
17		a. amplifying DNA from said individual and DNA
18		from said sample with a primer pair specific
19		for an HLA locus under suitable conditions to
20		produce an amplified DNA sequence from said
21		individual and from said sample, said primers
22		being located in intervening sequences I and
23		III for an HLA Class I locus and in
24		intervening sequences I and II for a Class II
25		locus;
26		b. combining said amplified DNA sequence from
27		said individual and said amplified sample DNA
28		from said sample with at least one
29		endonuclease that cleaves said amplified DNA
30		sequence into a plurality of cleaved
31		sequences of sufficiently different lengths
32		to distinguish between alleles of said HLA
33		locus for a period of time sufficient for
34		digestion of said amplified DNA to produce a

digest; and



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1		TCCCCGGCGACCTATAGGAGATGG; CTAGGACCACCCATGTGACCAGC;
2		ATCTCCTCAGACGCCGAGATGCGTCAC;
3		CTCCTGCTGCTCTGGGGGGCAG; ACTTTACCTCCACTCAGATCAGGAG;
4		CGTCCAGGCTGTCTGGGTTCTGTGCCCCT;
5		CTGGTCACATGGGTGGTCCTAGG;
6		CGCCTGAATTTTCTGACTCTTCCCAT;
7		ATCCCGGGAGATCTACAGGAGATG; AACAGCGCCCATGTGACCATCCT;
8		CTGGGGAGGCGCCGCGTTGAGGATTCT;
9		CGTCTCCGCAGTCCCGGTTCTAAAGTTCCCAGT;
10		ATCCTCGTGCTCTCGGGA; TGTGGTCAGGCTGCTGAC;
11		AAGGTTTGATTCCAGCTT;
12		CCCCTTCCCCACCCCAGGTGTTCCTGTCCATTCTTCAGGA;
13		CACATGGGCGCTGTTGGAGTGTCG; GTGAGTGCGGGGGTCGGGAGGGA;
14		CACCCACCGGGACTCAGA; TGGCCCTGACCCAGACCTGGGC;
15		GAGGGTCGGGCGGTCTCAGC; CTCTCAGGCCTTGTTC;
16		CAGAAGTCGCTGTTCC; TTCTGAGCCAGTCCTGAGA;
17		TTGCCCTGACCACCGTGATG; CTTCCTGCTTGTCATCTTCA;
18		CCATGAATTTGATGGAGA; ACCGCTGCTACCAATGGTA;
19		CCAAGAGGTCCCCAGATC; TCATCATAGCTGTGCTGATG;
20		AGAACATGTGATCATCCAGGC; CCAACTATACTCCGATCACCAAT;
21		TGACAGTGACACTGATGGTGCTG; GGGGACACCCGACCACGTTTC;
22		TGCAGACAACTACGGGGTTG; TGGCTGAGGGCAGAGACTCTCCC;
23		TGCTACTTCACCAACGGGAC; GGTGTGCACACAACTAC;
24		AGGTATTTTACCCAGGGACCAAGAGAT;
25		ATGTAAAATCAGCCCGACTGCCTCTTC;
26		GCCTCGTGCCTTATGCGTTTGCCTCCT;
27		TGAGGTTAATAAACTGGAGAA; GAGAGTGGCGCCTCCGCTCAT; and
28		GAGTGAGGGCTTTGGGCCGG.
29	30.	An HLA Class I locus-specific primer pair.
30	31.	An HLA Class II locus-specific, intron-spanning
31		primer pair.
32	32.	A DNA sequence defined by an HLA locus-specific
33		primer pair.
34	33.	A kit comprising at least one HLA locus-specific
35		primer pair in a suitable container, wherein said
36		HLA locus-specific primer pair is selected from

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